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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/934,778

DATE: 09/10/2001

TIME: 09:01:54

Input Set : A:\17920SEQ.txt

Output Set: N:\CRF3\09102001\I934778.raw

3 <110> APPLICANT: Croteau, Rodney B
4 Burke, Charles C
6 <120> TITLE OF INVENTION: GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS
7 OF USE
9 <130> FILE REFERENCE: WSR117920
11 <140> CURRENT APPLICATION NUMBER: US/09/934,778
12 <141> CURRENT FILING DATE: 2001-08-21
14 <150> PRIOR APPLICATION NUMBER: 09/420,211
15 <151> PRIOR FILING DATE: 1999-10-18
17 <150> PRIOR APPLICATION NUMBER: PCT/US98/21772
18 <151> PRIOR FILING DATE: 1998-10-15
20 <150> PRIOR APPLICATION NUMBER: 08/951,924
21 <151> PRIOR FILING DATE: 1997-10-16
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1131
29 <212> TYPE: DNA
30 <213> ORGANISM: Mentha piperita
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1131)
36 <400> SEQUENCE: 1
37 atg agt gct ctt gtt aat cct gtg gcg aaa tgg cct cag acg atc ggc 48
38 Met Ser Ala Leu Val Asn Pro Val Ala Lys Trp Pro Gln Thr Ile Gly
39 1 5 10 15
41 gtt aaa gat gtt cac ggc ggc cgg agg cgg aga tcc aga tcc act ctc 96
42 Val Lys Asp Val His Gly Gly Arg Arg Arg Arg Ser Arg Ser Thr Leu
43 20 25 30
45 ttt caa tcc cat cca ctt cgc act gaa atg cct ttc tct ctc tac ttc 144
46 Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe
47 35 40 45
49 tca tcc ccc ctc aaa gct ccc gcc act ttt tcc gtt tct gca gtt tat 192
50 Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr
51 50 55 60
53 acc aaa gag ggc agc gaa att agg gat aaa gat ccg gcg cct tcg act 240
54 Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr
55 65 70 75 80
57 tcg ccg gcg ttc gat ttc gac gga tac atg ctc cgg aag gcg aaa tcc 288
58 Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser
59 85 90 95
61 gtc aac aag gcg ttg gaa gcg gcg gtg cag atg aag gag ccg ctg aag 336
62 Val Asn Lys Ala Leu Glu Ala Ala Val Gln Met Lys Glu Pro Leu Lys
63 100 105 110
65 atc cac gag tcc atg cgg tac tcc ctt ctc gcc gcc ggc aag aga gtg 384
66 Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val
67 115 120 125

ENTERED

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69 cgt cct atg ctg tgc atc gcg gcc tgc gag ctc gtc ggc ggc gac gag 432
70 Arg Pro Met Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Asp Glu
71 130 135 140
73 tcc acg gcg atg ccg gcg gcc tgc gcc gtc gag atg atc cac acg atg 480
74 Ser Thr Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr Met
75 145 150 155 160
77 tcg ctg atg cac gac gac ctc cca tgc atg gac aac gac gac ctc cgc 528
78 Ser Leu Met His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg
79 165 170 175
81 cgc ggc aag ccg acg aac cac atg gct ttc ggc gag agc gtg gcg gtc 576
82 Arg Gly Lys Pro Thr Asn His Met Ala Phe Gly Glu Ser Val Ala Val
83 180 185 190
85 ctc gcc ggc gac gcc ctc ctc tcc ttc gcg ttc gag cac gtg gcg gcg 624
86 Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Val Ala Ala
87 195 200 205
89 gcg acc aaa ggc gcg ccg ccg gag cgg atc gtg agg gtc ctc ggc gag 672
90 Ala Thr Lys Gly Ala Pro Pro Glu Arg Ile Val Arg Val Leu Gly Glu
91 210 215 220
93 ctg gct gtc tcg atc ggg tcg gag ggg ctg gtg gcg ggg cag gtg gtg 720
94 Leu Ala Val Ser Ile Gly Ser Glu Gly Leu Val Ala Gly Gln Val Val
95 225 230 235 240
97 gac gtc tgc tcg gag ggg atg gcg gag gtc ggg ctg gac cac ctc gag 768
98 Asp Val Cys Ser Glu Gly Met Ala Glu Val Gly Leu Asp His Leu Glu
99 245 250 255
101 ttc atc cac cac cac aag acg gcg gcg ctg ctg cag ggg tcg gtg gtt 816
102 Phe Ile His His His Lys Thr Ala Ala Leu Leu Gln Gly Ser Val Val
103 260 265 270
105 ctg ggg gcg att ttg ggc ggc gga aag gag gag gag gtg gcg aag ctg 864
106 Leu Gly Ala Ile Leu Gly Gly Gly Lys Glu Glu Glu Val Ala Lys Leu
107 275 280 285
109 aga aaa ttc gcg aat tgc atc gga ttg ctg ttt cag gtg gtg gac gat 912
110 Arg Lys Phe Ala Asn Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp
111 290 295 300
113 atc cta gat gtg acg aaa tcg tcc aag gaa ttg ggg aag acg gcg ggg 960
114 Ile Leu Asp Val Thr Lys Ser Ser Lys Glu Leu Gly Lys Thr Ala Gly
115 305 310 315 320
117 aag gat ctg gtg gcg gat aaa acc aca tat ccg aag cta ata ggc gtg 1008
118 Lys Asp Leu Val Ala Asp Lys Thr Thr Tyr Pro Lys Leu Ile Gly Val
119 325 330 335
121 gag aaa tcc aag gaa ttc gcg gat cgg ttg aac agg gag gcg cag gag 1056
122 Glu Lys Ser Lys Glu Phe Ala Asp Arg Leu Asn Arg Glu Ala Gln Glu
123 340 345 350
125 cag ctc ctc cat ttt cat cct cat agg gca gct cca ttg att gct ctc 1104
126 Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu
127 355 360 365
129 gcc aat tat att gct tat agg gac aat 1131
130 Ala Asn Tyr Ile Ala Tyr Arg Asp Asn
131 370 375
134 <210> SEQ ID NO: 2

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135 <211> LENGTH: 377
136 <212> TYPE: PRT
137 <213> ORGANISM: Mentha piperita
139 <400> SEQUENCE: 2
140 Met Ser Ala Leu Val Asn Pro Val Ala Lys Trp Pro Gln Thr Ile Gly
141   1           5           10           15
143 Val Lys Asp Val His Gly Gly Arg Arg Arg Arg Ser Arg Ser Thr Leu
144           20           25           30
146 Phe Gln Ser His Pro Leu Arg Thr Glu Met Pro Phe Ser Leu Tyr Phe
147           35           40           45
149 Ser Ser Pro Leu Lys Ala Pro Ala Thr Phe Ser Val Ser Ala Val Tyr
150           50           55           60
152 Thr Lys Glu Gly Ser Glu Ile Arg Asp Lys Asp Pro Ala Pro Ser Thr
153   65           70           75           80
155 Ser Pro Ala Phe Asp Phe Asp Gly Tyr Met Leu Arg Lys Ala Lys Ser
156           85           90           95
158 Val Asn Lys Ala Leu Glu Ala Ala Val Gln Met Lys Glu Pro Leu Lys
159           100          105          110
161 Ile His Glu Ser Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys Arg Val
162           115          120          125
164 Arg Pro Met Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly Asp Glu
165           130          135          140
167 Ser Thr Ala Met Pro Ala Ala Cys Ala Val Glu Met Ile His Thr Met
168   145          150          155          160
170 Ser Leu Met His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp Leu Arg
171           165          170          175
173 Arg Gly Lys Pro Thr Asn His Met Ala Phe Gly Glu Ser Val Ala Val
174           180          185          190
176 Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Val Ala Ala
177           195          200          205
179 Ala Thr Lys Gly Ala Pro Pro Glu Arg Ile Val Arg Val Leu Gly Glu
180           210          215          220
182 Leu Ala Val Ser Ile Gly Ser Glu Gly Leu Val Ala Gly Gln Val Val
183   225          230          235          240
185 Asp Val Cys Ser Glu Gly Met Ala Glu Val Gly Leu Asp His Leu Glu
186           245          250          255
188 Phe Ile His His His Lys Thr Ala Ala Leu Leu Gln Gly Ser Val Val
189           260          265          270
191 Leu Gly Ala Ile Leu Gly Gly Gly Lys Glu Glu Glu Val Ala Lys Leu
192           275          280          285
194 Arg Lys Phe Ala Asn Cys Ile Gly Leu Leu Phe Gln Val Val Asp Asp
195           290          295          300
197 Ile Leu Asp Val Thr Lys Ser Ser Lys Glu Leu Gly Lys Thr Ala Gly
198   305          310          315          320
200 Lys Asp Leu Val Ala Asp Lys Thr Thr Tyr Pro Lys Leu Ile Gly Val
201           325          330          335
203 Glu Lys Ser Lys Glu Phe Ala Asp Arg Leu Asn Arg Glu Ala Gln Glu
204           340          345          350
206 Gln Leu Leu His Phe His Pro His Arg Ala Ala Pro Leu Ile Ala Leu

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207          355          360          365
209 Ala Asn Tyr Ile Ala Tyr Arg Asp Asn
210          370          375
213 <210> SEQ ID NO: 3
214 <211> LENGTH: 5
215 <212> TYPE: PRT
216 <213> ORGANISM: Mentha piperita
218 <400> SEQUENCE: 3
219 Leu Ile Gly Val Glu
220 1 5
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 5
225 <212> TYPE: PRT
226 <213> ORGANISM: Mentha piperita
228 <400> SEQUENCE: 4
229 Tyr Ile Ala Tyr Arg
230 1 5
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 15
235 <212> TYPE: PRT
236 <213> ORGANISM: Mentha piperita
238 <400> SEQUENCE: 5
239 Thr Ala Ala Leu Leu Thr Gly Ser Val Val Leu Gly Ala Ile Leu
240 1 5 10 15
243 <210> SEQ ID NO: 6
244 <211> LENGTH: 9
245 <212> TYPE: PRT
246 <213> ORGANISM: Mentha piperita
248 <400> SEQUENCE: 6
249 Glu Ala Val Glu Thr Leu Leu His Phe
250 1 5
253 <210> SEQ ID NO: 7
254 <211> LENGTH: 26
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence ✓
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence:
260 oligonucleotide ✓
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature
264 <222> LOCATION: (1)..(26)
265 <223> OTHER INFORMATION: PCR primer GG23F
267 <400> SEQUENCE: 7
268 gaattgcatc ggattgctgt ttcagg 26
271 <210> SEQ ID NO: 8
272 <211> LENGTH: 24
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:

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277 <223> OTHER INFORMATION: Description of Artificial Sequence:
278     oligonucleotide
280 <220> FEATURE:
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (1)..(24)
283 <223> OTHER INFORMATION: PCR primer GG23R
285 <400> SEQUENCE: 8
286 ccgccaccag atccttcccc gccg                                     24
289 <210> SEQ ID NO: 9
290 <211> LENGTH: 101
291 <212> TYPE: DNA
292 <213> ORGANISM: Mentha piperita
294 <400> SEQUENCE: 9
295 cgaattgcat cggattgctg tttcaggtgg tggacgatat cctagatgtg acgaaatcgt 60
297 ccaaggaatt ggggaagacg gcggggaagg atctggtggc g                               101
300 <210> SEQ ID NO: 10
301 <211> LENGTH: 1131
302 <212> TYPE: DNA
303 <213> ORGANISM: Mentha piperita
305 <220> FEATURE:
306 <221> NAME/KEY: CDS
307 <222> LOCATION: (6)..(944)
309 <400> SEQUENCE: 10
310 tcaaa atg gcc att aat ctc tcc cat atc aac tcc aaa aca tgt ttc cct 50
311     Met Ala Ile Asn Leu Ser His Ile Asn Ser Lys Thr Cys Phe Pro
312         1             5             10             15
314 ctc aaa aca aga tct gat ctc agc cgt tct tct tcc gcg cgt tgc atg 98
315 Leu Lys Thr Arg Ser Asp Leu Ser Arg Ser Ser Ser Ala Arg Cys Met
316             20             25             30
318 cca act gcc gcc gct gcc gcc ttc ccc act atc gcc acc gcc gcc caa 146
319 Pro Thr Ala Ala Ala Ala Phe Pro Thr Ile Ala Thr Ala Ala Gln
320             35             40             45
322 agt cag ccg tac tgg gcc gcc atc gag gcc gac ata gag aga tac ctg 194
323 Ser Gln Pro Tyr Trp Ala Ala Ile Glu Ala Asp Ile Glu Arg Tyr Leu
324             50             55             60
326 aag aaa tcc atc aca ata agg ccg ccg gag aca gtt ttc ggg ccc atg 242
327 Lys Lys Ser Ile Thr Ile Arg Pro Pro Glu Thr Val Phe Gly Pro Met
328             65             70             75
330 cac cac ctc acc ttc gcc gcc cca gcc acc gcc gcc tcc acc cta tgc 290
331 His His Leu Thr Phe Ala Ala Pro Ala Thr Ala Ala Ser Thr Leu Cys
332 80             85             90             95
334 ttg gcg gcg tgc gag ctc gtc ggc ggc gac cga agc caa gcc atg gca 338
335 Leu Ala Ala Cys Glu Leu Val Gly Gly Asp Arg Ser Gln Ala Met Ala
336             100             105             110
338 gcc gcg gcg gcg atc cat ctc gtg cac gcg gca gcc tac gtc cac gag 386
339 Ala Ala Ala Ala Ile His Leu Val His Ala Ala Ala Tyr Val His Glu
340             115             120             125
342 cac ctc cct cta acc gac ggg tcg agg ccc gta tcc aag ccc gca atc 434
343 His Leu Pro Leu Thr Asp Gly Ser Arg Pro Val Ser Lys Pro Ala Ile

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15